# SEQ SEARCH SUMMARY

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 20, 2003, 19:02:39 ; Search time 4689 Seconds

(without alignments)

16594.180 Million cell updates/sec

Title:

US-09-824-551-1

Perfect score: 1902

Sequence:

1 ggtaggagtaaaaacgcag.....ggccccggcgtccaaggaac 1902

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched:

2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*

- 1: gb ba:\*
- 2: gb\_htg:\*
- 3: gb\_in:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb sy:\*
- 13: gb un:\*
- 14: gb\_vi:\*
- 15: em ba:\*
- 16: em fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
- 19: em\_mu:\*
- 20: em om:\*
- 21: em\_or:\*
- 22: em\_ov:\*
- 23: em\_pat:\*
- 24: em ph:\*
- 25: em\_pl:\*
- 26: em\_ro:\*
- 27: em\_sts:\*

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28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_rod:*
36: em_htg_wam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Res	No.	Score	Query Match Length	DB	ID	Description
	1	1902	100.0 1902	6	AX397915 WO 02/20799 Rathe	AX397915 Sequence
	2	1902	100.0 1902	6	AX398211 No 02/20793 "	AX398211 Sequence
C	3	1902	100.0 309400	6	AX127153 EP 1108790 Nakagawa	-AX127153 Sequence
С	4	1902	100.0 325651	1	AP005283 Gentlenk	AP005283 Corynebac
	5	1311	68.9 1311		AX123323 <i>EP</i>	AX123323 Sequence
	6	1311	68.9 1311		BD165440 JP - Nakagawa	BD165440 Novel pol
С	7	773.2	40.7 302070		AP005223	AP005223 Corynebac
C	8	639	33.6 639		AX123321	AX123321 Sequence
С	9	639	33.6 639	6	BD165438	BD165438 Novel pol
	10	404	21.2 1052		AX377471	AX377471 Sequence
C	11	319	16.8 588	6	AX123322	AX123322 Sequence
С	12	319	16.8 588		BD165439 AX065953 Promoving WO 01/00842	BD165439 Novel pol
	13	291	15.3 759		AX065953 Pompejus 600 01/00842	AX065953 Sequence
	14	191	10.0 636		AX123320	AX123320 Sequence
	15	191	10.0 636	6	BD165437	BD165437 Novel pol
	16	108	5.7 339650	1	SC0939108	AL939108 Streptomy
	17	96.4	5.1 1149	6	AX122285	AX122285 Sequence
	18	96.4	5.1 1149	6	BD164402	BD164402 Novel pol
С	19	96.4	5.1 337200	1	AP005280	AP005280 Corynebac
C	20	96.4	5.1 349980	6	AX127149	AX127149 Sequence
С	21	96.4	5.1 349980	6	AX127150	AX127150 Sequence
	22	76.6	4.0 299050	1	SCO939119	AL939119 Streptomy
	23	73.2	3.8 2760	1	SRSENRS	Y14336 Streptomyce
С	24	70.8	3.7 298450	1	SCO939107	AL939107 Streptomy
	25	70.4	3.7 10035	1	AE001999	AE001999 Deinococc
С	26	63.8	3.4 291000	1	SC0939105	AL939105 Streptomy
C	27	61.6	3.2 255447	2	AC096032	AC096032 Rattus no
	28	61	3.2 1965	1	BSU18135	U18135 Pseudomonas
C	29	61	3.2 196050	1	AL646058	AL646058 Ralstonia
	30	60.6	3.2 632	6	AX435920	AX435920 Sequence
	31	60.6	3.2 299925	1	AP005043	AP005043 Streptomy
	32	60.4	3.2 753	6	AX065957	AX065957 Sequence
	33	60.4	3.2 1032	6	AX376724	AX376724 Sequence

OM nucleic - nucleic search, using sw model

October 20, 2003, 18:19:14; Search time 385 Seconds Run on:

(without alignments)

13335.925 Million cell updates/sec

Title: US-09-824-551-1

Perfect score: 1902

Sequence: 1 qqtaqqaqtaaaaaacqcaq.....gqccccqqcqtccaaqqaac 1902

IDENTITY NUC Scoring table:

Gapop 10.0 , Gapext 1.0

Searched: 2552756 segs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 19Jun03:\*

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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*

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/SIDS1/gcgdata/geneseg/genesegn-emb1/NA1985.DAT:\* 6:

7: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\* /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*

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/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:\* 19:

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24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

25: /SIDS1/gcgdata/geneseg/genesegn-emb1/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.   Score   Match Length DB   ID   Description				ક			5011111(1110)	
1   1902   100.0   1902   24   ABL40476   20   207494   C.   glutamicum codin codin   3   1311   68.9   1311   22   AAR68534   27   107279   C.   glutamicum codin   68.9   1311   22   AAR68534   27   107279   C.   glutamicum codin   C.   64   658   45.1   858   25   ACA01369   C.   glutamicum codin   C.   64   64   64   64   64   64   64   6	Res	3111+						
1	1101		Score		Length	DB	TD	Dosgription
C 2 1902 100.0 309400 22 AAH68534 & Institute of the color of the colo								Description
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3 1311 68.9 1311 22 AAH68204 C glutamicum codin   6 415 21.8 426 25 ACA01379 C. glutamicum codin   6 415 21.8 426 25 ACA01379 C. glutamicum codin   7 404 21.2 1052 24 ABA91930 Corynebacterium gl   C 8 319 16.8 588 22 AAH68203 C glutamicum codin   9 291 15.3 759 22 AAF71286 Corynebacterium gl   C 10 280 14.7 549 25 ACA01390 C. glutamicum codin   11 191 10.0 636 22 AAH68201 C glutamicum codin   12 96.4 5.1 1149 22 AAH68201 C glutamicum codin   12 96.4 5.1 349980 22 AAH68531 C glutamicum codin   15 60.6 3.2 632 24 ABA91930 C glutamicum codin   16 60.4 3.2 753 22 AAF71288 Corynebacterium gl   17 60.4 3.2 1032 24 ABA95154 C. glutamicum codin   18 60 3.2 630 22 AAH67165 C glutamicum codin   19 58.2 3.1 2538 20 AAX21398 Central fragment o   20 58.2 3.1 155074 24 ABN85735 Human genomic regi   15 6.2 3.0 12531 23 AAS59530 Propionibacterium   21 56.2 3.0 12531 23 AAS59604 Propionibacterium   22 53.4 2.8 233 24 ABN23371 Human ORFX polynuc   23 53 2.8 353 24 ABN23371 Human ORFX polynuc   24 52.6 52 2.7 29736 22 AAF88314 S. spinosa DNA fra   25 52 2.7 29736 22 AAF88314 S. spinosa DNA fra   27 51.6 2.7 601 24 ABK77051 Bacillus lichenifo   28 51 2.7 840 22 AAS63305 DNA encoding novel   28 51 2.7 840 22 AAS63305 DNA encoding novel   33 48 2.5 1058 24 ABK79656 Bacillus lichenifo   34 48 2.5 1058 24 ABK79656 Bacillus lichenifo   35 46.8 2.5 1058 24 ABK79666 Bacillus lichenifo   36 46.8 2.5 6693 23 ABS2979 Drosophila melanog   37 46.8 2.5 6693 23 ABS2979 Drosophila melanog   38 46.8 2.5 662 23 AAS9330 PNA encoding novel   40 46.6 2.5 642 19 AAV39839 Pseudomonas fluore   40 46.6 2.5 642 19 AAV39839 Pseudomonas fluore   41 46.6 2.5 642 19 AAV39839 Pseudomonas fluore   42 46.6 2.5 642 19 AAV39839 Pseudomonas fluore   44 46.4 2.4 1635 22 ABA9946 Human breast cell	С	2	1902	100.0				C alutamicum codin
C   S   G39   33.6   G39   22   AAR68202   C   Glutamicum deri		3	1311					
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C 37 46.8 2.5 486 22 AAF75507 Polyglutamine trac 38 46.8 2.5 1122 23 AAS93196 DNA encoding novel 40 46.6 2.5 642 19 AAV39839 Pseudomonas fluore 41 46.6 2.5 642 19 AAV31652 Nucleotide sequenc 42 46.6 2.5 642 20 AAX99370 P. fluorescens mod 46.6 2.5 2109 23 AAS81477 DNA encoding novel 46.4 2.4 1635 22 ABA49946 Human breast cell								
38 46.8 2.5 1122 23 AAS93196 DNA encoding novel c 39 46.8 2.5 3297 23 AAS91437 DNA encoding novel 40 46.6 2.5 642 19 AAV39839 Pseudomonas fluore 41 46.6 2.5 642 19 AAV31652 Nucleotide sequenc 42 46.6 2.5 642 20 AAX99370 P. fluorescens mod c 43 46.6 2.5 2109 23 AAS81477 DNA encoding novel c 44 46.4 2.4 1635 22 ABA49946 Human breast cell								_
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40 46.6 2.5 642 19 AAV39839 Pseudomonas fluore 41 46.6 2.5 642 19 AAV31652 Nucleotide sequenc 42 46.6 2.5 642 20 AAX99370 P. fluorescens mod c 43 46.6 2.5 2109 23 AAS81477 DNA encoding novel c 44 46.4 2.4 1635 22 ABA49946 Human breast cell	С							
41 46.6 2.5 642 19 AAV31652 Nucleotide sequenc 42 46.6 2.5 642 20 AAX99370 P. fluorescens mod c 43 46.6 2.5 2109 23 AAS81477 DNA encoding novel c 44 46.4 2.4 1635 22 ABA49946 Human breast cell	_							
42 46.6 2.5 642 20 AAX99370 P. fluorescens mod c 43 46.6 2.5 2109 23 AAS81477 DNA encoding novel c 44 46.4 2.4 1635 22 ABA49946 Human breast cell								
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c 44 46.4 2.4 1635 22 ABA49946 Human breast cell	C							
numan bleast cell								
Human foetal liver								
	_	4 J	7 U • 4	۷.4	1033	44	C0810ADA	Human foetal liver

OM nucleic - nucleic search, using sw model

Run on: October 20, 2003, 20:40:15; Search time 376 Seconds

(without alignments)

13284.296 Million cell updates/sec

Title: US-09-824-551-1

Perfect score: 1902

Sequence: 1 ggtaggagtaaaaaacgcag.....ggccccggcgtccaaggaac 1902

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1750203 seqs, 1313063994 residues

Total number of hits satisfying chosen parameters: 3500406

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications NA:\*

1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*

2: /cgn2 6/ptodata/2/pubpna/PCT NEW PUB.seq:\*

3: /cgn2 6/ptodata/2/pubpna/US06 NEW PUB.seq:\*

4: /cgn2 6/ptodata/2/pubpna/US06 PUBCOMB.seq:\*

5: /cgn2 6/ptodata/2/pubpna/US07 NEW PUB.seq:\*

6: /cgn2\_6/ptodata/2/pubpna/PCTUS PUBCOMB.seq:\*

7: /cgn2\_6/ptodata/2/pubpna/US08 NEW PUB.seq:\*

8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*

9: /cgn2 6/ptodata/2/pubpna/US09A PUBCOMB.seq:\*

10: /cgn2 6/ptodata/2/pubpna/US09B PUBCOMB.seq:\*

11: /cgn2 6/ptodata/2/pubpna/US09C PUBCOMB.seq:\*

12: /cgn2 6/ptodata/2/pubpna/US09 NEW PUB.seq:\*

13: /cgn2\_6/ptodata/2/pubpna/US10A PUBCOMB.seq:\*

14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*

15: /cgn2 6/ptodata/2/pubpna/US10 NEW PUB.seq:\*

16: /cgn2 6/ptodata/2/pubpna/US60 NEW PUB.seq:\*

17: /cgn2 6/ptodata/2/pubpna/US60 PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result Query No. Score Match Length DB ID Description \_\_\_\_\_\_ ------1902 100.0 3309400 10 US-09-738-626-1 Mokagawa Sequence 1, Appli Sequence 1 7001 1902 100.0 1902 10 US-09-824-551-1 HEFE 1 Sequence 1, Appli 68.9 1311 10 US-09-738-626-3239 Sequence 3239, Ap 3 1311 639 33.6 639 10 US-09-738-626-3237 Sequence 3237, Ap С 4 Sequence 3238, Ap 5 . 319 16.8 588 10 US-09-738-626-3238 С 10.0 636 10 US-09-738-626-3236 191 Sequence 3236, Ap 6 10 US-09-738-626-2201 V 7 1149 Sequence 2201, Ap 96.4 5.1 8 60.6 3.2 632 10 US-09-974-300-4335 Sequence 4335, Ap 9 60.6 3.2 717 14 US-10-156-761-5606 Sequence 5606, Ap 60.6 3.2 9025608 14 US-10-156-761-1 Sequence 1, Appli 10 11 60.4 3.2 1032 11 US-09-867-537A-1 Sequence 1, Appli 12 60 3.2 630 10 US-09-738-626-2200 Sequence 2200, Ap 13 58.2 3.1 155074 13 US-10-026-188-6 Sequence 6, Appli Sequence 2864, Ap 14 57.2 3.0 639 14 US-10-156-761-2864 15 57.2 3.0 9025608 14 US-10-156-761-1 Sequence 1, Appli 2.9 16 55.6 663 14 US-10-156-761-1453 Sequence 1453, Ap 17 55.2 2.9 639 14 US-10-156-761-6454 Sequence 6454, Ap 18 681 14 US-10-156-761-6016 53.6 2.8 Sequence 6016, Ap 19 53.2 2.8 669 14 US-10-156-761-1976 Sequence 1976, Ap 20 51.6 2.7 601 10 US-09-974-300-4342 Sequence 4342, Ap 2.6 14 US-10-077-584-3 Sequence 3, Appli 21 50 1236 С 22 48.2 2.5 669 14 US-10-156-761-4665 Sequence 4665, Ap 2.5 1058 10 US-09-974-300-4257 23 48 Sequence 4257, Ap 47.2 2.5 744 14 US-10-156-761-5052 24 Sequence 5052, Ap 25 47 2.5 648 14 US-10-156-761-4438 Sequence 4438, Ap 26 47 2.5 1972 12 US-10-017-161-1981 Sequence 1981, Ap 27 46.6 2.5 672 14 US-10-156-761-4521 Sequence 4521, Ap 1635 9 US-09-864-761-20241 c 28 46.4 2.4 Sequence 20241, A 1973 9 US-09-864-761-3471 c 29 46.4 2.4 Sequence 3471, Ap 669 14 US-10-156-761-7370 30 46.2 2.4 Sequence 7370, Ap 2.4 38918 12 US-10-017-161-2049 31 45.8 Sequence 2049, Ap 32 45.6 2.4 672 14 US-10-156-761-4519 Sequence 4519, Ap 33 1075 9 US-09-864-761-19241 45.6 2.4 Sequence 19241, A 34 45.6 1403 9 US-09-864-761-2513 2.4 Sequence 2513, Ap 35 45.4 2.4 88421 10 US-09-976-059-1 C Sequence 1, Appli 612 14 US-10-156-761-3119 36 45 2.4 Sequence 3119, Ap 37 45 2.4 3367 12 US-09-890-688-129 Sequence 129, App 5085 14 US-10-198-846-9854 38 45 2.4 Sequence 9854, Ap 39 45 2.4 5499 14 US-10-198-846-12674 Sequence 12674, A 40 44.4 2.3 446 9 US-09-864-761-20699 Sequence 20699, A 1104 9 US-09-815-242-6579 41 43.8 2.3 Sequence 6579, Ap 2.3 10391 10 US-09-070-927A-133 42 43.8 Sequence 133, App 729 14 US-10-156-761-3236 43 2.3 Sequence 3236, Ap 43 9 US-09-815-242-9828 44 42.8 2.3 720 Sequence 9828, Ap 45 42.8 2.3 1234 12 US-10-182-504-1 Sequence 1, Appli

OM nucleic - nucleic search, using sw model

October 20, 2003, 19:21:29; Search time 2764 Seconds Run on:

(without alignments)

16724.715 Million cell updates/sec

Title: US-09-824-551-1

Perfect score: 1902

1 ggtaggagtaaaaacgcag.....ggccccggcgtccaaggaac 1902 Sequence:

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

22781392 seqs, 12152238056 residues Searched:

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

1: em estba:\*

2: em esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em estro:\*

8: em\_htc:\*

9: gb est1:\*

10: gb est2:\*

11: gb htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em estfun:\*

16: em estom:\* 17: em\_gss hum:\*

18: em\_gss\_inv:\*

19: em gss pln:\*

20: em gss vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em gss mus:\*

24: em gss pro:\*

25: em gss\_rod:\*

26: em gss\_phg:\*

27: em gss\_vrl:\* 28: gb gss1:\*

# 29: gb\_gss2:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Res	sult		Query				
	No.	Score		Length	DB	ID	Description
							Description
С	1	57	3.0	644	12	BM605179	BM605179 170006870
	2	56.6	3.0	712	13	BX416727	BX416727 BX416727
	3	55	2.9	885	13	BX425603	BX425603 BX425603
	4	54.8	2.9	895	29	CNS0071A	AL066286 Drosophil
	5	50.8	2.7	884	29	CNS006U0	AL065923 Drosophil
C	6	50.6	2.7	818	29	BZ229437	BZ229437 CH230-401
C	7	50.2	2.6	570	14	CD344209	CD344209 EtESTef78
С	8	49.4	2.6	638	13	BW260725	BW260725 BW260725
C	9	49.4	2.6	712	28	ВН898573	BH898573 MB61p8H7
	10	49.2	2.6	711	28	BZ098560	BZ098560 CH230-235
	11	49.2	2.6	922	29	CNS0073W	AL066784 Drosophil
С	12	48.8	2.6	1005	29	CNS02LA1	AL202546 Tetraodon
	13	48.8	2.6	1132	29	BZ559201	
С	14	48.4	2.5	711	12	BM588321	BZ559201 pacs2-164 BM588321 170006873
	15	48.2	2.5	439	12	BJ348296	
	16	48.2	2.5	468	12	BJ348080	BJ348296 BJ348296
	17	48.2	2.5	505	12	BJ406583	BJ348080 BJ348080
	18	48.2	2.5	522	12	BJ353136	BJ406583 BJ406583
	19	48.2	2.5	555	12	BJ403974	BJ353136 BJ353136
	20	48.2	2.5	695	12	BJ439038	BJ403974 BJ403974
С	21	48	2.5	664	12	BM595824	BJ439038 BJ439038
C	22	47.8	2.5	540		AW464269	BM595824 170006874
0	23	47.6	2.5	689	12		AW464269 BP230015A
	24	47.2	2.5	902	29	BJ485119	BJ485119 BJ485119
	25	47.2	2.5	1201	13	CNS006QP	AL065804 Drosophil
С	26	47.2	2.5	789	28	BX356664	BX356664 BX356664
c	27	46.6	2.5	494	28 12	BZ115869	BZ115869 CH230-255
C	28	46.4	2.4			BM641696	BM641696 170006873
c	29	46.4	2.4	450	14	CA915472	CA915472 PCS01853X
С	30	46.4		481	14	CA915480	CA915480 PCS04158
C	31	46.4	2.4	506	14	CA899712	CA899712 PCEP01447
C	32		2.4	512	14	CA915525	CA915525 PCSC21474
c	33	46.4	2.4	598	14	CA915510	CA915510 PCSC17379
		46.4	2.4	617	13	BW314712	BW314712 BW314712
C	34	46.4	2.4	638	12	BM618697	BM618697 170006874
C	35	46.4	2.4	699	12	BM630395	BM630395 170006875
C	36	46.2	2.4	796	29	BZ556455	BZ556455 pacs1-60_
C	37	46	2.4	572	29	CNS043SN	AL273200 Tetraodon
C	38	46	2.4	602	13	BW192111	BW192111 BW192111
C	39	46	2.4	603	14	CB555832	CB555832 MMSP0006_
C	40	46	2.4	621	13	BW265801	BW265801 BW265801
C	41	46	2.4	658	13	BW265514	BW265514 BW265514
С	42	46	2.4	663	13	BW259047	BW259047 BW259047
	43	45.8	2.4	477	14	CA743784	CA743784 wrils.pk0
6	4 4 4 E	45.8	2.4	585	13	BQ190440	BQ190440 UI-R-DN1-
С	45	45.6	2.4	560	14	CD569824	CD569824 EtESTeg05

OM nucleic - nucleic search, using sw model

Run on: October 20, 2003, 19:23:55; Search time 100 Seconds

(without alignments)

8395.107 Million cell updates/sec

Title: US-09-824-551-1

Perfect score: 1902

Sequence: 1 ggtaggagtaaaaacgcag.....ggccccggcgtccaaggaac 1902

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*

6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Res	ult		% Ouerv				
	No.	Score	- 4	Length	DB	ID	Description
	1	60.4	3.2	1032	4	US-09-897-537A-1	Sequence 1, Appli
	2	58.2	3.1	2588	2	US-08-796-414B-6	Sequence 6, Appli
	3	51	2.7	840	4	US-09-651-656-106	Sequence 106, App
	4	51	2.7	840	4	US-09-650-855-106	Sequence 106, App
	5	48.8	2.6	678	4	US-09-252-991A-794	Sequence 794, App
C	6	48.8	2.6	867	4	US-09-252-991A-848	Sequence 848, App
С	7	48.8	2.6	2577	4	US-09-252-991A-828	Sequence 828, App
	8	48.4	2.5	810	4	US-09-252-991A-3647	Sequence 3647, Ap
	9	48.4	2.5	879	4	US-09-252-991A-3602	Sequence 3602, Ap
С	10	48.4	2.5	1632	4	US-09-252-991A-3859	Sequence 3859, Ap
	11	46.6	2.5	642	1	US-08-761-258-4	Sequence 4, Appli

OM nucleic - nucleic search, using sw model

Run on: October 20, 2003, 21:28:31; Search time 4688 Seconds

(without alignments)

16597.720 Million cell updates/sec

US-09-824-551-1 Title:

Perfect score: 1902

1 ggtaggagtaaaaaacgcag.....ggccccggcgtccaaggaac 1902 Sequence:

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

2888711 seqs, 20454813386 residues Searched:

Word size :

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:\*

1: gb ba:\*

2: gb htg:\*

3: gb in:\*

4: gb om:\*

5: gb\_ov:\*

6: gb\_pat:\* 7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb ro:\*

11: gb sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vi:\*

15: em\_ba:\*

16: em\_fun:\*

17: em hum:\*

18: em in:\*

19: em mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em ph:\*

25: em\_pl:\*

26: em ro:\*

27: em sts:\*

28: em un:\*

```
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36:
     em htg mam: *
37:
    em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40:
    em_htgo_mus:*
    em_htgo_other:*
41:
```

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Res	ult No.	Score	Query Match	Length	DB	ID	Description
	1	1902	100.0	1902	6	AX397915	AX397915 Sequence
	2	1902	100.0	1902	6	AX398211	AX398211 Sequence
С	3	1902	100.0	309400	6	AX127153	AX127153 Sequence
C	4	1902	100.0	325651	1	AP005283	AP005283 Corynebac
	5	1311	68.9	1311	6	AX123323	AX123323 Sequence
	6	1311	68.9	1311	6	BD165440	BD165440 Novel pol
С	7	639	33.6	639	6	AX123321	AX123321 Sequence
С	8	639	33.6	639	6	BD165438	BD165438 Novel pol
	9	404	21.2	1052	6	AX377471	AX377471 Sequence
C	10	319	16.8	588	6	AX123322	AX123322 Sequence
C	11	319	16.8	588	6	BD165439	BD165439 Novel pol
	12	291	15.3	759	6	AX065953	AX065953 Sequence
	13	191	10.0	636	6	AX123320	AX123320 Sequence
	14	191	10.0	636	6	BD165437	BD165437 Novel pol
	15	53	2.8	353	6	AX377473	AX377473 Sequence
C	16	35	1.8	302070	1	AP005223	AP005223 Corynebac
	17	23	1.2	121358	9	AF228727	AF228727 Homo sapi
C	18	23	1.2	179892	2	AC087820	AC087820 Homo sapi
C	19	23	1.2	183687	9	AC009622	AC009622 Homo sapi
C	20	22		161424	2	AC018367	AC018367 Homo sapi
	21	22		162495	2	AC015647	AC015647 Homo sapi
	22	22	1.2	198714	9	CNS05TDW	AL357172 Human chr
	23	22	1.2	202212	9	CNS01RGF	AL157957 Human chr
С	24	21	1.1	68329	2	AC101548	AC101548 Mus muscu
С	25	21		149567	10	AC136639	AC136639 Mus muscu
C	26	21		154090	2	AC144580	AC144580 Mus muscu
C	27	21		156629	2	AC141629	AC141629 Mus muscu
	28	21		166631	2	AC131770	AC131770 Mus muscu
	29	21		170607	2	AC116502	AC116502 Mus muscu
С	30	21		175475	2	AC123631	AC123631 Mus muscu
С	31	21		182444	2	AC116481	AC116481 Mus muscu
C	32	21		185452	2	AC114566	AC114566 Mus muscu
	33	21		187381	2	AC135667	AC135667 Mus muscu
C	34	21	1.1	190309	10	AC121771	AC121771 Mus muscu

OM nucleic - nucleic search, using sw model

October 20, 2003, 21:26:30 ; Search time 387 Seconds Run on:

(without alignments)

13267.006 Million cell updates/sec

Title: US-09-824-551-1

Perfect score: 1902

1 ggtaggagtaaaaacgcag.....ggccccggcgtccaaggaac 1902 Sequence:

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

2552756 seqs, 1349719017 residues Searched:

Word size :

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N Geneseq 19Jun03:\*

1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*

2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*

3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*

4: /SIDS1/gcgdata/geneseg/genesegn-emb1/NA1983.DAT:\*

/SIDS1/gcgdata/geneseg/genesegn-emb1/NA1984.DAT:\*

/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*

7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:\*

8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:\*

9: /SIDS1/qcqdata/qeneseq/qeneseqn-embl/NA1988.DAT:\*

10: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*

11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:\* 12:

/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:\*

13: /SIDS1/gcgdata/geneseg/genesegn-emb1/NA1992.DAT:\*

14: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\* 15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:\*

16:

/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:\*

17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:\*

18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:\* 19:

/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\* 20: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:\*

21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:\*

22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*

23:

/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\* 24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

-	2 .		%				
Re	sult No.	Score	Query	Length	DΒ	ID	Description
	1	1902	100.0	1902	24	ABL40476	C. glutamicum luxS
С	2	1902	100.0	309400	22	AAH68534	C glutamicum codin
	3	1311	68.9	1311	22	AAH68204	C glutamicum codin
	4	858	45.1	858	25	ACA01369	C. glutamicum deri
С	5	639	33.6	639	22	AAH68202	C glutamicum codin
	6	411	21.6	426	25	ACA01379	C. glutamicum deri
	7	404	21.2	1052	24	ABA91930	Corynebacterium gl
С	8	319	16.8	588	22	AAH68203	C glutamicum codin
	9	291	15.3	759	22	AAF71286	Corynebacterium gl
С	10	280	14.7	549	25	ACA01390	C. glutamicum deri
	11	191	10.0	636	22	AAH68201	C glutamicum codin
	12	53	2.8	353	24	ABA91931	Corynebacterium gl
	13	20	1.1	20	24	ABL40477	C. glutamicum luxS
С	14	20	1.1	20	24	ABL40478	C. glutamicum luxS
	15	20	1.1	20	24	ABA91932	Corynebacterium gl
С	16	20	1.1	382	14	AAQ59551	Human brain Expres
С	17	20	1.1	1323	24	ABK98540	Botulinum neurotox
С	18	20	1.1	1323	24	ABK98550	Botulinum neurotox
C	19	20	1.1	2475	24	ABK98551	Botulinum neurotox
	20	20	1.1	4827	22	AAI59592	Human polynucleoti
С	21	20	1.1	9486	23	AAS66084	DNA encoding novel
	22	20	1.1	9486	23	AAS90982	DNA encoding novel
С	23	20	1.1	10196	24	AAI64255	Human SLC5A3 gene
C	24	20	1.1	10302	24	AAI72720	BCW2 cDNA. Homo s
С	25	20	1.1	23213	24	ABV78027	Hypoxia-regulated
C	26	19	1.0	383	25	ABX45609	Bovine EST associa
C	27	19	1.0	559	21	AAA31333	Plant microsatelli
С	28	19	1.0	1108	22	AAF71333	Corynebacterium gl
С	29	19	1.0	1116	22	AAH67595	C glutamicum codin
	30	19	1.0	1999	24	ABQ61023	FLJ22833 fis clone
С	31	19	1.0	2811	23	ABL25174	Drosophila melanog
С	32	19	1.0	30390	23	AAS59520	Propionibacterium
	33	19	1.0	349980	22	AAH68532	C glutamicum codin
C	34	18	0.9	264	25	ABX23491	Human GDP-mannose
С	35	18	0.9	490	22	AAK76336	Human immune/haema
С	36	18	0.9	496	22	AAK59840	Human immune/haema
С	37	18	0.9	653	21	AAF12197	Aspergillus oryzae
	38	18	0.9	658	24	ABX65502	Helicobacter pylor
	39	18	0.9	672	23	ABL13199	Drosophila melanog
	40	18	0.9	723	22	AAH67475	C glutamicum codin
	41	18	0.9	723	25	ACA01224	C. glutamicum deri
C	42	18	0.9	969	25	ACA01000	C. glutamicum deri
С	43	18	0.9	978	22	AAH66424	C glutamicum codin
	44	18	0.9	1001	21	AAC57967	Arachidonic acid m
	45	18	0.9	1021	24	ABX66099	Helicobacter pylor

OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 00:13:12; Search time 373 Seconds

(without alignments)

13391.141 Million cell updates/sec

Title: US-09-824-551-1

Perfect score: 1902

Sequence: 1 ggtaggagtaaaaaacgcag.....ggccccggcgtccaaggaac 1902

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 1750203 segs, 1313063994 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3500406

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: Published Applications NA:\*

1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*

2: /cgn2 6/ptodata/2/pubpna/PCT NEW PUB.seq:\*

3: /cgn2 6/ptodata/2/pubpna/US06 NEW PUB.seq:\*

4: /cgn2 6/ptodata/2/pubpna/US06 PUBCOMB.seq:\*

5: /cgn2 6/ptodata/2/pubpna/US07 NEW PUB.seq:\*

6: /cgn2\_6/ptodata/2/pubpna/PCTUS PUBCOMB.seq:\*

7: /cgn2 6/ptodata/2/pubpna/US08 NEW PUB.seq:\*

8: /cgn2 6/ptodata/2/pubpna/US08 PUBCOMB.seq:\*

9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*

10: /cgn2 6/ptodata/2/pubpna/US09B PUBCOMB.seq:\*

11: /cgn2 6/ptodata/2/pubpna/US09C PUBCOMB.seq:\*

10. / cg/12\_0/pcodaca/2/pabpina/05090\_roboonb.seq.

12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*

13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq: \*

14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*

15: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
16: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

17: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Des	1 ±		%				
Res	Sult No.	Score	Query	Length	מח	TD	<b>D</b>
		20016		Length	лв 	ID	Description
	1	1902	100.0	1902	10	US-09-824-551-1	Sequence 1, Appli
C	2	1902		3309400			Sequence 1, Appli
	3	1311	68.9	1311	10	US-09-738-626-3239	Sequence 3239, Ap
C	4	639	33.6	639	10	US-09-738-626-3237	Sequence 3237, Ap
C	5	319	16.8	588	10	US-09-738-626-3238	Sequence 3238, Ap
	6	191	10.0	636	10	US-09-738-626-3236	Sequence 3236, Ap
	7	22	1.2	516	13	US-10-027-632-287113	Sequence 287113,
С	8	21	1.1	3138	14	US-10-156-761-2538	Sequence 2538, Ap
	9	21	1.1	9025608	14	US-10-156-761-1	Sequence 1, Appli
	10	20	1.1	20	10	US-09-824-551-3	Sequence 3, Appli
С	11	20	1.1	20	10	US-09-824-551-4	Sequence 4, Appli
С	12	20	1.1	1323	13	US-10-011-588-10	Sequence 10, Appl
С	13	20	1.1		13	US-10-011-588-30	Sequence 30, Appl
C	14	20	1.1	2475	13	US-10-011-588-32	Sequence 32, Appl
С	15	19	1.0	383	10	US-09-960-352-10774	Sequence 10774, A
С	16	19	1.0	611	13	US-10-027-632-192050	Sequence 192050,
C	17	19	1.0	961	13	US-10-027-632-251784	Sequence 251784,
C	18	19	1.0	1116	10	US-09-738-626-2630	Sequence 2630, Ap
	19	19	1.0	3309400	10	US-09-738-626-1	Sequence 1, Appli
C	20	18	0.9	261	14	US-10-156-761-494	Sequence 494, App
C	21	18	0.9	264	10	US-09-878-574-5550	Sequence 5550, Ap
C	22	18	0.9	461	14	US-10-171-581-314	Sequence 314, App
С	23	18	0.9	536	13	US-10-027-632-136635	Sequence 136635,
С	24	. 18	0.9	687	13	US-10-027-632-106927	Sequence 106927,
С	25	18	0.9	687	13	US-10-027-632-106928	Sequence 106928,
С	26	18	0.9	687	13	US-10-027-632-136634	Sequence 136634,
	27	18	0.9	723	10	US-09-738-626-2510	Sequence 2510, Ap
С	28	18	0.9	727	13	US-10-027-632-25349	Sequence 25349, A
С	29	18	0.9	727	13	US-10-027-632-25350	Sequence 25350, A
	30	18	0.9	800	13	US-10-027-632-154095	Sequence 154095,
С	31	18	0.9	931	12	US-10-017-161-1863	Sequence 1863, Ap
C	32	18	0.9	978	10	US-09-738-626-1459	Sequence 1459, Ap
С	33	18	0.9	1079	14	US-10-078-090-3	Sequence 3, Appli
	34 35	18	0.9	1468	12	US-09-882-227-259	Sequence 259, App
~	36	18	0.9	2007	10	US-09-801-368-237	Sequence 237, App
С		18	0.9	3393	14	US-10-128-714-203	Sequence 203, App
~	37 38	18	0.9	3401	14	US-10-081-119-19	Sequence 19, Appl
C		18	0.9	3867	14	US-10-128-714-202	Sequence 202, App
С	39 40	18 18	0.9	4035	14	US-10-128-714-5202	Sequence 5202, Ap
			0.9	13584	12	US-10-311-455-587	Sequence 587, App
C	41 42	18 18		536165	11	US-09-939-964-1	Sequence 1, Appli
c c	43	18		1830121	14	US-10-329-960-1	Sequence 1, Appli
C	43	18 17		9025608	14	US-10-156-761-1	Sequence 1, Appli
	45	17 17	0.9 0.9		10	US-09-783-590-8947	Sequence 8947, Ap
	4 J	Τ,	0.9	186	10	US-09-878-574-3194	Sequence 3194, Ap

ALIGNMENTS

OM nucleic - nucleic search, using sw model

October 20, 2003, 22:36:02; Search time 2765 Seconds Run on:

(without alignments)

16718.667 Million cell updates/sec

US-09-824-551-1 Title:

Perfect score: 1902

1 ggtaggagtaaaaaacgcag.....ggccccggcgtccaaggaac 1902 Sequence:

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

22781392 segs, 12152238056 residues Searched:

Word size :

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:\*

1: em estba:\*

2: em esthum:\*

3: em estin:\*

4: em estmu:\*

5: em\_estov:\*
6: em\_estpl:\*

7: em\_estro:\*

8: em htc:\*

9: gb est1:\*

10: gb est2:\*

11: gb htc:\*

12: gb est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em estfun:\*

16: em\_estom:\*

17: em\_gss hum:\*

18: em gss inv:\*

19: em gss pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em gss rod:\*

26: em gss phg:\*

27: em gss vrl:\*

28: gb\_gss1:\* 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

						SUMMAKI	FO
			of				
Res	sult		Query				
	No.	Score	Match	Length	DB	ID	Description
			1 0		1.0		D2010515 TTO 178007
	1	23	1.2	383	10	BF910515	BF910515 IL2-UT007
С	2	22	1.2	591	29	BZ492878	BZ492878 BONBP91TF
С	3	22	1.2	856	29	BZ497273	BZ497273 BONSE69TR
	4	21	1.1	345	28	BH265149	BH265149 CH230-55I
С	5	21	1.1	642	29	BX192671	BX192671 Danio rer
	6	21	1.1	767	28	AZ717195	AZ717195 RPCI-24-1
	7	21	1.1	805	29	BZ209421	BZ209421 CH230-342
	8	20	1.1	192	28	BH174645	BH174645 Bir49L18
C	9	20	1.1	273	10	BF716978	BF716978 NcEST3a19
C	10	20	1.1	273	14	N88922	N88922 K6584F Huma
	11	20	1.1	292	28	AZ007734	AZ007734 RPCI-23-2
C	12	20	1.1	382	14	м78393	M78393 EST00541 Fe
	13	20	1.1	394	12	BI058627	BI058627 CM3-GN029
C	14	20	1.1	485	12	BI515786	BI515786 BB160020B
C	15	20	1.1	486	28	AZ009964	AZ009964 RPCI-23-2
	16	20	1.1	659	14	CB267786	СВ267786 1006692 Н
С	17	20	1.1	746	29	AG134951	AG134951 Pan trogl
C	18	20	1.1	859	29	CC400720	CC400720 PUHLM18TD
C	19	20	1.1	936	29	BZ571963	BZ571963 msh2 2170
С	20	20	1.1	1058	12	BM562952	BM562952 AGENCOURT
С	21	20	1.1	1543	29	CC208526	CC208526 CH261-108
С	22	19	1.0	256	12	BI293206	BI293206 UI-R-DK0-
	23	19	1.0	331	9	AA375611	AA375611 EST88182
С	24	19	1.0	359	9	AL968593	AL968593 AL968593
	25	19	1.0	368	9	AA781849	AA781849 ai61g09.s
С	26	19	1.0	414	9	AV690055	AV690055 AV690055
	27	19	1.0	416	13	BY208181	BY208181 BY208181
	28	19	1.0	418	10	BE493362	BE493362 WHE0571 H
	29	19	1.0	422	6	AL812086	Al812086 Triticum
С	30	19	1.0	427	13	BQ529073	BQ529073 3524 1 44
	31	19	1.0	432	13	BY281892	BY281892 BY281892
С	32	19	1.0	436	9	AL786619	AL786619 AL786619
	33	19	1.0	457	13	BY561821	BY561821 BY561821
	34	19	1.0	458	10	BF717012	BF717012 NcEST3a19
	35	19	1.0	459	12	BM147775	BM147775 TCAAP1Q14
С	36	19	1.0			AL645006	AL645006 AL645006
c	37	19	1.0	467	13	BX088966	BX088966 BX088966
Ŭ	38	19	1.0	476	9	AA147562	AA147562 zl51d01.r
С	39	19	1.0	483	14	CA826740	CA826740 1114004C1
c	40	19	1.0	495	13	BQ442032	BQ442032 3524 1 7
C	41	19	1.0	503	9	AV604523	AV604523 AV604523
С	42	19	1.0	503	13	BU097610	BU097610 3524 1 19
	43	19	1.0	505	9	AW418953	AW418953 ha24d06.x
C	44	19	1.0	503	9	AL801184	AW416955 NAZ4400.X AL801184 AL801184
C	45	19	1.0	507	9	AL801184 AL970492	AL801184 AL801184 AL970492 AL970492
С	40	1.0	1.0	508	J	AU3/0434	MU3/0432 AU3/0432

OM nucleic - nucleic search, using sw model

Run on: October 20, 2003, 22:41:31; Search time 102 Seconds

(without alignments)

8230.497 Million cell updates/sec

Title: US-09-824-551-1

Perfect score: 1902

Sequence: 1 ggtaggagtaaaaaacgcag.....ggccccggcgtccaaggaac 1902

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:\*

1: /cgn2 6/ptodata/2/ina/5A COMB.seq:\*

2: /cgn2 6/ptodata/2/ina/5B COMB.seq:\*

3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*

4: /cgn2 6/ptodata/2/ina/6B COMB.seg:\*

5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*

6: /cgn2 6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ult No.	Score	% Query Match	Length	DB	ID	Description
	1	18	0.9	657	4	US-09-252-991A-7507	Sequence 7507, Ap
	2	18	0.9	1001	4	US-09-641-638-601	Sequence 601, App
C	3	18	0.9	1185	4	US-09-252-991A-1931	Sequence 1931, Ap
	4	18	0.9	1287	4	US-09-252-991A-7363	Sequence 7363, Ap
C	5	18	0.9	1392	4	US-09-252-991A-7136	Sequence 7136, Ap
C	6	18	0.9	2163	3	US-09-296-284-22	Sequence 22, Appl
C	7	18	0.9	2232	5	PCT-US96-05320A-113	Sequence 113, App
C	8	18	0.9	2265	3	US-09-296-284-1	Sequence 1, Appli
C	9	18	0.9	4830	3	US-09-296-284-7	Sequence 7, Appli
	10	18	0.9	536165	4	US-09-214-808-1	Sequence 1, Appli
C	11	18	0.9	1830121	4	US-09-557-884-1	Sequence 1, Appli